

# SEQUENCE LISTING

<110> Duffy, Hao-Peng Xu  
 <120> Identification of Differentially Methylated  
 And Mutated Nucleic Acids  
 <130> 52494/1903  
 <140> filed concurrently herewith  
 <141> 1999-06-30  
 <150> 08/657,866  
 <151> 1996-05-31  
 <160> 16  
 <170> WordPerfect 6.1 for Windows

<210> 1  
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<400> 7

ccggggccccc acaggccccg tgctgaaaca gggctggaac caggcaactt gtttctttgt 60  
cctgacatcc ctgcgcagct ggtaccgagt ggacagcccc aacaaactca tgaacccgct 120  
ggtcgctggg gtcttcggag ccattgtggg agcggccagt gtcttcggaa atgctcctct 180  
gcacgagatc gagccccaga tgcgggacct ggaggtgcac aaatgcataa cacatgggac 240  
tgtggctgca aatcctgagg gaagggcaca agaccttctt acaagggcac tattgcccgc 300  
ctgggcccgg 309

<210> 8

<211> 332

<212> DNA

<213> Homo sapiens

<400> 8

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tgcccagtggt gcaatcttcc cagatggggc ttctgccaca cattcacgtc tgatctggca 120  
gggtgtttctt ctgccaaacc ttcctccttc tcggatgctc ttctgccaca tgtgcaatcc 180  
tgtcagacgt tcctgpcact cgaggtagct ggtctgatgt gagcatggaa ccaggggggtc 240  
cccctaccac caccaggaat gtcagatgat catgaggtgt cggttgggcg gttcttgaac 300  
cctatctatg gaggataacc gctcacggcc gg 332

<210> 9

<211> 568

<212> DNA

<213> Homo sapiens

<400> 9

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gcgggagggt actgggggtg gaagtggaag aaggtggcac agtaacagac tcccttctcc 180  
tgagattccc agcatggatt ggaggggctg ccctgcagcg tccettaccc cttgttacct 240  
ggcagcctgc aagtagctct agggccagcc atgtggtcac ctacatctgt tgggggagag 300  
aaggaaaaca gatgccccga gtcgtagaga cttgcattat cagcccctgg gtccaacagc 360  
aagtgagcta agcacttgca aatgttatct gatgtattct ttataagaag gggtcacaaa 420  
actgagactt agaacatgta agagggagac agggatttga gcctggatca gctatgtgag 480  
gatctcctgt ctgtccccgc tggttccaat tcaggtctta gagtaaaagg gttggggatg 540  
agctctctgg caggacagtg ccctccgg 568

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<211> 1005

<212> DNA

<213> Homo sapiens

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aggctgcatt catgattttc aatagacctg tgatggtctg tgcccagtgc tggggacaca 120  
gaagagtcaa acctggctcc tgacctggac ctggatcatc acgtgacagg gaggagagcg 180  
atccaggctg atgaggaaag cgcattgacat ggggtcttag gagcagtgag gggcagagcc 240  
atggccaaag gccccgcat ggaagctgag gactctggca ccagatggag gcagttgacc 300  
gacctctgcc cttgggggtcc aacctatggg cttctcatac ataggggtga aaaaggccat 360  
tctatttatg cagaattttc ccatgtggcc aggcagcaga agtccagagg ggtaggggcc 420

actcaggggtc acacagaaca gcagttgctg aagactgggg aagtccaggc ctaggctcca 480  
 cctgcccttc cctgacatg gggccaccac tagcctttta tgggcaggcc tggttgctgg 540  
 tggttggaat aacatctgac tccagtgggt gtctgtcacc gtctccagac aggagacaga 600  
 gacagaggggt caaagttcac tatggctctt tggggcaatg aaatgctgtg ttctagcctc 660  
 ttgccagaaa tcagccaaag tcaaggaaag cctgactccc acagttatca cagaaagagc 720  
 acccactttc cagcccagac agctgcaccc cagctgggtc ctggcagccc cagcttcagc 780  
 ctgggcggtta tgttccaggc cctcgatca tctgacccta atatcacccc ttcacacccc 840  
 ctccactttc tgcgggagcc acccgaacc tttgaatggg ggagatcctg gaggctctgc 900  
 aattttcagt gtaaactgcc tggagtcccc cacttcaccc tcatctgggt cacctgtgga 960  
 ctccaacag agcaggccca ggaaacgcgg ggcctctgag gccgg 1005

<210> 11

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic primer

<400> 11

cctggatggt cagcgtg

17

<210> 12

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic primer

<400> 12

cagtgttggt aggaggag

18

<210> 13

<211> 682

<212> DNA

<213> Homo Sapiens

<220>

<223> Synthetic probe

<400> 13

cctggatggt cagcgtgagg gccaatggca cacacatctg tgccggcacc atcattgcct 60

cccagtgggt gctgactgtg gccactgcc tgatctggcg tgatgttacc tactcagtga 120

gggtggggag tccgtggatt gaccagatga cgcagaccgc ctccgatgtc ccggtgctcc 180

aggtcatcat gcatagcagg taccggggcc agcgggtctg gtccctgggtg ggccaggcca 240

acgacatcgg cctcctcaag ctcaagcagg aactcaagta cagcaattac gtgcggccca 300

tctgcctgcc tggcacggac tatgtgttga aggaccattc ccgctgcact gtgacgggct 360

ggggactttc caaggctgac ggcatgtggc ctgagttccg gaccattcag gagaaggaag 420

tcatcatcct gaacaacaaa gagtgtgaca atttctacca caacttcacc aaaatcccca 480

ctctgggttca gatcatcaag tcccagatga tgtgtgcgga ggacaccac aggagagaag 540

tctgctatga gctaactgga gagcccttgg tctgctccat ggagggcacg tggtagctgg 600

tgggattggt gagctggggt gcaggctgcc agaagagcga ggccccaccc atctacctac 660

aggtctcctc ctaccaacac tg 682

<210> 14

<211> 1240

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 60..1214

<220>

<223> cDNA

<400> 14

gtcgtggggg cggcactggg agcgccttcc ggagagacgc agtcggctgc caccgccggg 59

atg ggt cgc tgg tgc cag acc gtc gcg cgc ggg cag cgc ccc cgg acg 107  
Met Gly Arg Trp Cys Gln Thr Val Ala Arg Gly Gln Arg Pro Arg Thr  
5 10 15

tct gcc ccc tcc cgc gcc ggt gcc ctg ctg ctg ctg ctt ctg ttg ctg 155  
Ser Ala Pro Ser Arg Ala Gly Ala Leu Leu Leu Leu Leu Leu Leu  
20 25 30

agg tct gca ggt tgc tgg ggc gca ggg gaa gcc ccg ggg gcg ctg tcc 203  
Arg Ser Ala Gly Cys Trp Gly Ala Gly Glu Ala Pro Gly Ala Leu Ser  
35 40 45

act gct gat ccc gcc gac cag agc gtc cag tgt gtc ccc aag gcc acc 251  
Thr Ala Asp Pro Ala Asp Gln Ser Val Gln Cys Val Pro Lys Ala Thr  
50 55 60

tgt cct tcc agc cgg cct cgc ctt ctc tgg cag acc ccg acc acc cag 299  
Cys Pro Ser Ser Arg Pro Arg Leu Leu Trp Gln Thr Pro Thr Thr Gln  
65 70 75 80

aca ctg ccc tcg acc acc atg gag acc caa ttc cca gtt tct gaa ggc 347  
Thr Leu Pro Ser Thr Thr Met Glu Thr Gln Phe Pro Val Ser Glu Gly  
85 90 95

aaa gtc gac cca tac cgc tcc tgt ggc ttt tcc tac gag cag gac ccc 395  
Lys Val Asp Pro tyr Arg Ser Cys Gly Phe Ser tyr Glu Gln Asp Pro  
100 105 110

acc ctc agg gac cca gaa gcc gtg gct cgg cgg tgg ccc tgg atg gtc	443
Thr Leu Arg Asp Pro Glu Ala Val Ala Arg Arg Trp Pro Trp Met Val	
115 120 125	
agc gtg cgg gcc aat ggc aca cac atc tgt gcc ggc acc atc att gcc	491
Ser Val Arg Ala Asn Gly Thr His Ile Cys Ala Gly Thr Ile Ile Ala	
130 135 140	
tcc cag tgg gtg ctg act gtg gcc cac tgc ctg atc tgg cgt gat gtt	539
Ser Gln Trp Val Leu Thr Val Ala His Cys Leu Ile Trp Arg Asp Val	
145 150 155 160	
atc tac tca gtg agg gtg ggg agt ccg tgg att gac cag atg acg cag	587
Ile tyr Ser Val Arg Val Gly Ser Pro Trp Ile Asp Gln Met Thr Gln	
165 170 175	
acc gcc tcc gat gtc ccg gtg ctc cag gtc atc atg cat agc agg tac	635
Thr Ala Ser Asp Val Pro Val Leu Gln Val Ile Met His Ser Arg Tyr	
180 185 190	
cgg gcc cag cgg ttc tgg tcc tgg gtg ggc cag gcc aac gac atc ggc	683
Arg Ala Gln Arg Phe Trp Ser Trp Val Gly Gln Ala Asn Asp Ile Gly	
195 200 205	
ctc ctc aag ctc aag cag gaa ctc aag tac agc aat tac gtg cgg ccc	731
Leu Leu Lys Leu Lys Gln Glu Leu Lys tyr Ser Asn tyr Val Arg Pro	
210 215 220	
atc tgc ctg cct ggc acg gac tat gtg ttg aag gac cat tcc cgc tgc	779
Ile Cys Leu Pro Gly Thr Asp tyr Val Leu Lys Asp His Ser Arg Cys	
225 230 235 240	
act gtg acg ggc tgg gga ctt tcc aag gct gac ggc atg tgg cct cag	827
Thr Val Thr Gly Trp Gly Leu Ser Lys Ala Asp Gly Met Trp Pro Gln	
245 250 255	



ttc cgg acc att cag gag aag gaa gtc atc atc ctg aac aac aaa gag	875
Phe Arg Thr Ile Gln Glu Lys Glu Val Ile Ile Leu Asn Asn Lys Glu	
260 265 270	
tgt gac aat ttc tac cac aac ttc acc aaa atc ccc act ctg gtt cag	923
Cys Asp Asn Phe tyr His Asn Phe Thr Lys Ile Pro Thr Leu Val Gln	
275 280 285	
atc atc aag tcc cag atg atg tgt gcg gag gac acc cac agg gag aag	971
Ile Ile Lys Ser Gln Met Met Cys Ala Glu Asp Thr His Arg Glu Lys	
290 295 300	
ttc tgc tat gag cta act gga gag ccc ttg gtc tgc tcc atg gag ggc	1019
Phe Cys tyr Glu Leu Thr Gly Glu Pro Leu Val Cys Ser Met Glu Gly	
305 310 315 320	
acg tgg tac ctg gtg gga ttg gtg agc tgg ggt gca ggc tgc cag aag	1067
Thr Trp tyr Leu Val Gly Leu Val Ser Trp Gly Ala Gly Cys Gln Lys	
325 330 335	
agc gag gcc cca ccc atc tac cta cag gtc tcc tcc tac caa cac tgg	1115
Ser Glu Ala Pro Pro Ile tyr Leu Gln Val Ser Ser tyr Gln His Trp	
340 345 350	
atc tgg gac tgc ctc aac ggg cag gcc ctg gcc ctg cca gcc cca tcc	1163
Ile Trp Asp Cys Leu Asn Gly Gln Ala Leu Ala Leu Pro Ala Pro Ser	
355 360 365	
agg acc ctg ctc ctg gca ctc cca ctg ccc ctc agc ctc ctt gct gcc	1211
Arg Thr Leu Leu Leu Ala Leu Pro Leu Pro Leu Ser Leu Leu Ala Ala	
370 375 380	
ctc tgactctgtg tgccctccc tcacttg	1240
Leu	
385	

<210> 15

<211> 1155

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 1..1155

<220>

<223> coding region of cDNA

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Met Gly Arg Trp Cys Gln Thr Val Ala Arg Gly Gln Arg Pro Arg Thr	
5 10 15	

ctg ccc cct ccc gcg ccg gtg ccc tgc tgc tgc tgc ttc tgt tgc tga	96
Ser Ala Pro Ser Arg Ala Gly Ala Leu Leu Leu Leu Leu Leu Leu	
20 25 30	

ggt ctg cag gtt gct ggg gcg cag ggg aag ccc cgg ggg cgc tgt cca	144
Arg Ser Ala Gly Cys Trp Gly Ala Gly Glu Ala Pro Gly Ala Leu Ser	
35 40 45	

ctg ctg atc ccg ccg acc aga gcg tcc agt gtg tcc cca agg cca cct	192
Thr Ala Asp Pro Ala Asp Gln Ser Val Gln Cys Val Pro Lys Ala Thr	
50 55 60	

gtc ctt cca gcc ggc ctc gcc ttc tct ggc aga ccc cga cca ccc aga	240
Cys Pro Ser Ser Arg Pro Arg Leu Leu Trp Gln Thr Pro Thr Thr Gln	
65 70 75 80	

cac tgc cct cga cca cca tgg aga ccc aat tcc cag ttt ctg aag gca	288
Thr Leu Pro Ser Thr Thr Met Glu Thr Gln Phe Pro Val Ser Glu Gly	
85 90 95	

aag tcg acc cat acc gct cct gtg gct ttt cct acg agc agg acc cca	336
Lys Val Asp Pro tyr Arg Ser Cys Gly Phe Ser tyr Glu Gln Asp Pro	
100 105 110	
ccc tca ggg acc cag aag ccg tgg ctc ggc ggt ggc cct gga tgg tca	384
Thr Leu Arg Asp Pro Glu Ala Val Ala Arg Arg Trp Pro Trp Met Val	
115 120 125	
gcg tgc ggg cca atg gca cac aca tct gtg ccg gca cca tca ttg cct	432
Ser Val Arg Ala Asn Gly Thr His Ile Cys Ala Gly Thr Ile Ile Ala	
130 135 140	
ccc agt ggg tgc tga ctg tgg ccc act gcc tga tct ggc gtg atg tta	480
Ser Gln Trp Val Leu Thr Val Ala His Cys Leu Ile Trp Arg Asp Val	
145 150 155 160	
tct act cag tga ggg tgg gga gtc cgt gga ttg acc aga tga cgc aga	528
Ile tyr Ser Val Arg Val Gly Ser Pro Trp Ile Asp Gln Met Thr Gln	
165 170 175	
ccg cct ccg atg tcc cgg tgc tcc agg tca tca tgc ata gca ggt acc	576
Thr Ala Ser Asp Val Pro Val Leu Gln Val Ile Met His Ser Arg Tyr	
180 185 190	
ggg ccc agc ggt tct ggt cct ggg tgg gcc agg cca acg aca tcg gcc	624
Arg Ala Gln Arg Phe Trp Ser Trp Val Gly Gln Ala Asn Asp Ile Gly	
195 200 205	
tcc tca agc tca agc agg aac tca agt aca gca att acg tgc ggc cca	672
Leu Leu Lys Leu Lys Gln Glu Leu Lys tyr Ser Asn tyr Val Arg Pro	
210 215 220	
tct gcc tgc ctg gca cgg act atg tgt tga agg acc att ccc gct gca	720
Ile Cys Leu Pro Gly Thr Asp tyr Val Leu Lys Asp His Ser Arg Cys	
225 230 235 240	

ctg tga cgg gct ggg gac ttt cca agg ctg acg gca tgt ggc ctc agt	768
Thr Val Thr Gly Trp Gly Leu Ser Lys Ala Asp Gly Met Trp Pro Gln	
245 250 255	
tcc gga cca ttc agg aga agg aag tca tca tcc tga aca aca aag agt	816
Phe Arg Thr Ile Gln Glu Lys Glu Val Ile Ile Leu Asn Asn Lys Glu	
260 265 270	
gtg aca att tct acc aca act tca cca aaa tcc cca ctc tgg ttc aga	864
Cys Asp Asn Phe tyr His Asn Phe Thr Lys Ile Pro Thr Leu Val Gln	
275 280 285	
tca tca agt ccc aga tga tgt gtg cgg agg aca ccc aca ggg aga agt	912
Ile Ile Lys Ser Gln Met Met Cys Ala Glu Asp Thr His Arg Glu Lys	
290 295 300	
tct gct atg agc taa ctg gag agc cct tgg tct gct cca tgg agg gca	960
Phe Cys tyr Glu Leu Thr Gly Glu Pro Leu Val Cys Ser Met Glu Gly	
305 310 315 320	
cgt ggt acc tgg tgg gat tgg tga gct ggg gtg cag gct gcc aga aga	1008
Thr Trp tyr Leu Val Gly Leu Val Ser Trp Gly Ala Gly Cys Gln Lys	
325 330 335	
gcg agg ccc cac cca tct acc tac agg tct cct cct acc aac act gga	1056
Ser Glu Ala Pro Pro Ile tyr Leu Gln Val Ser Ser tyr Gln His Trp	
340 345 350	
tct ggg act gcc tca acg ggc agg ccc tgg ccc tgc cag ccc cat cca	1104
Ile Trp Asp Cys Leu Asn Gly Gln Ala Leu Ala Leu Pro Ala Pro Ser	
355 360 365	
gga ccc tgc tcc tgg cac tcc cac tgc ccc tca gcc tcc ttg ctg ccc	1152
Arg Thr Leu Leu Leu Ala Leu Pro Leu Pro Leu Ser Leu Leu Ala Ala	
370 375 380	

tct

Leu

385

&lt;210&gt; 16

&lt;211&gt; 385

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 16

Met Gly Arg Trp Cys Gln Thr Val Ala Arg Gly Gln Arg Pro Arg Thr  
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Ser Ala Pro Ser Arg Ala Gly Ala Leu Leu Leu Leu Leu Leu Leu Leu  
                                   20                                  25                                  30

Arg Ser Ala Gly Cys Trp Gly Ala Gly Glu Ala Pro Gly Ala Leu Ser  
                                   35                                  40                                  45

Thr Ala Asp Pro Ala Asp Gln Ser Val Gln Cys Val Pro Lys Ala Thr  
                                   50                                  55                                  60

Cys Pro Ser Ser Arg Pro Arg Leu Leu Trp Gln Thr Pro Thr Thr Gln  
                                   65                                  70                                  75                                  80

Thr Leu Pro Ser Thr Thr Met Glu Thr Gln Phe Pro Val Ser Glu Gly  
                                   85                                  90                                  95

Lys Val Asp Pro Tyr Arg Ser Cys Gly Phe Ser Tyr Glu Gln Asp Pro  
                                   100                                  105                                  110

Thr Leu Arg Asp Pro Glu Ala Val Ala Arg Arg Trp Pro Trp Met Val  
                                   115                                  120                                  125

Ser Val Arg Ala Asn Gly Thr His Ile Cys Ala Gly Thr Ile Ile Ala  
                                   130                                  135                                  140

Ser Gln Trp Val Leu Thr Val Ala His Cys Leu Ile Trp Arg Asp Val  
 145 150 155 160

Ile Tyr Ser Val Arg Val Gly Ser Pro Trp Ile Asp Gln Met Thr Gln  
 165 170 175

Thr Ala Ser Asp Val Pro Val Leu Gln Val Ile Met His Ser Arg Tyr  
 180 185 190

Arg Ala Gln Arg Phe Trp Ser Trp Val Gly Gln Ala Asn Asp Ile Gly  
 195 200 205

Leu Leu Lys Leu Lys Gln Glu Leu Lys Tyr Ser Asn Tyr Val Arg Pro  
 210 215 220

Ile Cys Leu Pro Gly Thr Asp Tyr Val Leu Lys Asp His Ser Arg Cys  
 225 230 235 240

Thr Val Thr Gly Trp Gly Leu Ser Lys Ala Asp Gly Met Trp Pro Gln  
 245 250 255

Phe Arg Thr Ile Gln Glu Lys Glu Val Ile Ile Leu Asn Asn Lys Glu  
 260 265 270

Cys Asp Asn Phe Tyr His Asn Phe Thr Lys Ile Pro Thr Leu Val Gln  
 275 280 285

Ile Ile Lys Ser Gln Met Met Cys Ala Glu Asp Thr His Arg Glu Lys  
 290 295 300

Phe Cys Tyr Glu Leu Thr Gly Glu Pro Leu Val Cys Ser Met Glu Gly  
 305 310 315 320

Thr Trp Tyr Leu Val Gly Leu Val Ser Trp Gly Ala Gly Cys Gln Lys  
 325 330 335

Ser Glu Ala Pro Pro Ile Tyr Leu Gln Val Ser Ser Tyr Gln His Trp

340

345

350

Ile Trp Asp Cys Leu Asn Gly Gln Ala Leu Ala Leu Pro Ala Pro Ser

355

360

365

Arg Thr Leu Leu Leu Ala Leu Pro Leu Pro Leu Ser Leu Leu Ala Ala

370

375

380

Leu

385